

SEQUENCE LISTING

<110> Maines, Mahin D.

<120> METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
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<150> 60/261,500

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<170> PatentIn Ver. 2.1

<210> 1

<211> 296

<212> PRT

<213> Homo sapiens

<400> 1

Met Asn Ala Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
1 5 10 15

Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
20 25 30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Gln Glu Leu Trp Glu
100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys
290 295

<210> 2

<211> 1070

<212> DNA

<213> Homo sapiens

<400> 2

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tccgtgcgga ttagggactt gcggaatcca cacccttcct cagcgttcct gaacctgatt 180
ggcttcgtgt cgagaaggga gctcgggagc attgatggag tccagcagat ttctttggag 240
gatgctctt ccagccaaga ggtggaggc gcctatatct gcagtggagag ctccagccat 300
gaggactaca tcagggcgtt ccttaatgct ggcaagcacf tccttggat ataccccatg 360
acactgtcat tggcggccgc tcaggaactg tgggagctgg ctgagcagaa agaaaaagtc 420

ttgcacgagg agcatgttga actcttgatg gaggaattcg ctttcctgaa aaaagaagtg 480
gtggggaaag acctgctgaa agggtcgctc ctcttcacat ctgaccggtt ggaagaagac 540
cggtttggct tccctgcatt cagcggcatc tctcgactga cctggctggt ctccctctt 600
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aaactctgg gccagttctc tgagaaggaa ctggctgctg aaaagaaaacg catcctgcac 900
tgc当地ggc ttgc当地aga aatccagaaa tattgctgtt caaggaagta agaggaggag 960
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<210> 3

<211> 296

<212> PRT

<213> Homo sapiens

<400> 3

Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
1 5 10 15

Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
20 25 30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
 165 170 175
 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
 180 185 190
 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
 195 200 205
 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
 210 215 220
 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
 225 230 235 240
 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
 245 250 255
 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
 260 265 270
 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
 275 280 285
 Gln Lys Tyr Cys Cys Ser Arg Lys
 290 295

 <210> 4
 <211> 295
 <212> PRT
 <213> Rattus norvegicus

 <400> 4
 Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
 1 5 10 15
 Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
 20 25 30
 Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
 35 40 45
 Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
 50 55 60
 Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu

65	70	75	80
Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu			
85	90	95	
Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu			
100	105	110	
Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu			
115	120	125	
Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu			
130	135	140	
Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg			
145	150	155	160
Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val			
165	170	175	
Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg			
180	185	190	
Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn			
195	200	205	
Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg			
210	215	220	
Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val			
225	230	235	240
Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile			
245	250	255	
Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala			
260	265	270	
Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln			
275	280	285	
Lys Leu Cys His Gln Lys Lys			
290	295		
<210> 5			
<211> 1081			
<212> DNA			

<213> Rattus norvegicus

<400> 5

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gaaatttgg a tggtagtgg ttgggttgg cagagctggc tcggtaggc tgagggactt 180
gaaggatcca cgctctgcag cattcctgaa cctgatttgg tttgttcca gacgagagct 240
tgggagcctt gatgaagtac ggcagattc ttggaaagat gctctccgaa gccaagagat 300
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gaacatttcc ctgaaagatc aggatattt tttcagaag ctcttagacc agtctctgc 900
agaggacccg gctgcgtgaga agaagcgcatttgc ctggggctgg ccagcgcacat 960
ccagaagctt tgccaccaga agaagtgaag aggaagcttc agagacttct gaagggggcc 1020
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a 1081

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: hydrophobic
domain of BVR

<220>

<221> PEPTIDE

<222> (2)

<223> where X is any aa

<400> 6

Phe Xaa Val Val Val Val

1

5

<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleotide
binding domain of BVR

<220>
<221> PEPTIDE
<222> (2)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (4)..(5)
<223> where X is any aa

<400> 7
Gly Xaa Gly Xaa Xaa Gly
1 5

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oxidoreductase domain of BVR

<400> 8
Ala Gly Leu His Val Leu Val Glu
1 5

<210> 9
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: leucine
zipper of BVR

<220>
<221> PEPTIDE
<222> (2)..(7)
<223> where X is any aa

<220>

<221> PEPTIDE
<222> (9)..(14)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (16)..(21)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (23)..(28)
<223> where X is any aa

<400> 9

Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Leu
20 25

<210> 10
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: kinase motif
of BVR

<400> 10
Ser Arg Arg
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<210> 11
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: kinase motif
of BVR

<400> 11
Lys Gly Ser
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<210> 12
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: kinase motif
of BVR

<220>
<221> PEPTIDE
<222> (3)
<223> where X is any aa

<400> 12
Phe Thr Xaa
1

<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nuclear
localization signal of BVR

<400> 13
Gly Leu Lys Arg Asn Arg Tyr
1 5

<210> 14
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: methylation
site of BVR

<400> 14
Pro Gly Leu Lys Arg
1 5

<210> 15
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: zinc finger
domain of BVR

<220>
<221> PEPTIDE
<222> (3)..(12)
<223> where X is any aa

<400> 15
His Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys
1 5 10

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: protein
kinase C enhancing domain

<220>
<221> PEPTIDE
<222> (5)
<223> where X is any aa

<400> 16
Lys Lys Arg Ile Xaa His Cys
1 5

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: protein
kinase C inhibiting domain

<220>
<221> PEPTIDE
<222> (3)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (5)..(7)
<223> where X is any aa

<400> 17

Gln Lys Xaa Cys Xaa Xaa Xaa Lys
1 5